

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Campbell, Robert K.
Jameson, Bradford A.
Chappel, Scott C.
- (ii) TITLE OF INVENTION: HYBRID PROTEINS
- (iii) NUMBER OF SEQUENCES: 22
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BROWDY AND NEIMARK
 - (B) STREET: 419 Seventh Street N.W., Ste. 300
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 22207
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/011,936
 - (B) FILING DATE: 20 February 1996
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Browdy, Roger L.
 - (B) REGISTRATION NUMBER: 25,618
 - (C) REFERENCE/DOCKET NUMBER: CAMPBELL=2A
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 - (A) TELEPHONE: (202) 628-5197
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1049 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 278..1047

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCCACATGGC TACAGGTAAG CGCCCCTAAA ATCCCTTTGG GCACAATGTG TCCTGAGGGG	60
AGAGGCAGCG ACCTGTAGAT GGGACGGGGG CACTAACCTT CAGGTTTGGG GCTTCTCAAT	120
CTCACTATCG CCATGTAAGC CCAGTATTTG GCCAATCTCA GAAAGCTCCT CCTCCCTGGA	180
GGGATGGAGA GAGAAAAACA AACAGCTCCT GGAGCAGGGA GAGTGCTGGC CTCTTGCTCT	240
CCGGCTCCCT CTGTTGCCCT CTGGTTTCTC CCCAGGC TCC CGG ACG TCC CTG CTC	295
Ser Arg Thr Ser Leu Leu	
1 5	

CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT GCC Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala 10 15 20	343
GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCC Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser 25 30 35	391
ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys 40 45 50	439
CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC TCC Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser 55 60 65 70	487
TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys 75 80 85	535
TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp 90 95 100	583
CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp 105 110 115	631
AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT GGG Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly 120 125 130	679
ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC TGC Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys 135 140 145 150	727
CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT GCC GGT His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ala Gly 155 160 165	775
GCT GCC CCA GGT TGC CCA GAA TGC ACG CTA CAG GAA AAC CCA TTC TTC Ala Ala Pro Gly Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe 170 175 180	823
TCC CAG CCG GGT GCC CCA ATA CTT CAG TGC ATG GGC TGC TGC TTC TCT Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser 185 190 195	871
AGA GCA TAT CCC ACT CCA CTA AGG TCC AAG AAG ACG ATG TTG GTC CAA Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln 200 205 210	919
AAG AAC GTC ACC TCA GAG TCC ACT TGC TGT GTA GCT AAA TCA TAT AAC Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn 215 220 225 230	967
AGG GTC ACA GTC ATG GGG GGT TTC AAA GTG GAG AAC CAC ACG GGG TGC Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His Thr Gly Cys 235 240 245	1015
CAC TGC AGT ACT TGT TAT TAT CAC AAA TCT TA AG His Cys Ser Thr Cys Tyr Tyr His Lys Ser 250 255	1049

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp
1 5 10 15
Leu Gln Glu Gly Ser Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile
20 25 30
His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr
35 40 45
Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg
50 55 60
Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His
65 70 75 80
Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile
85 90 95
Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn
100 105 110
Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys
115 120 125
Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln
130 135 140
Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu
145 150 155 160
Cys Val Ser Cys Ala Gly Ala Ala Pro Gly Cys Pro Glu Cys Thr Leu
165 170 175
Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys
180 185 190
Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys
195 200 205
Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys
210 215 220
Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val
225 230 235 240
Glu Asn His Thr Gly Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser
245 250 255

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 279..1199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCGAGATGG CTACAGGTAA GCGCCCCTAA AATCCCTTTG GGCACAATGT GTCCTGAGGG	60
GAGAGGTAGC GACCTGTAGA TGGGACGGGG GCACTAACCC TGAGGTTTGG GGCTTCTGAA	120
TGTGAGTATC GCCATGTAAG CCCAGTATTT GGCCAATGTC AGAAAGCTCC TGGTCCCTGG	180
AGGGATGGAG AGAGAAAAAC AAACAGCTCC TGGAGCAGGG AGAGTGCTGG CCTCTTGCTC	240
TCCGGCTCCC TCTGTTGCCC TGTGGTTTCT CCCCAGGC TCC CGG ACG TCC CTG	293
Ser Arg Thr Ser Leu	260
CTC CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT	341
Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser	265 270 275
GCC GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT	389
Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn	280 285 290
TCG ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC	437
Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp	295 300 305
TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC	485
Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly	310 315 320 325
TCT TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC	533
Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser	330 335 340
AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG	581
Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val	345 350 355
GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT	629
Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr	360 365 370
TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT	677
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn	375 380 385
GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC	725
Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr	390 395 400 405
TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT GCT	773
Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ala	410 415 420
GGT GCT GGT CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG	821
Gly Ala Gly Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala Val Glu	425 430 435
AAG GAG GGC TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC	869
Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala	440 445 450

GGC TAC TGC CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTC CCC GCC Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala 455 460 465	917
CTG CCT CAG GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile 470 475 480 485	965
CGG CTC CCT GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCT Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala 490 495 500	1013
GTG GCT CTC AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp 505 510 515	1061
TGC GGG GGT CCC AAG GAC CAC CCC TTG ACC TGT GAT GAC CCC CGC TTC Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp Asp Pro Arg Phe 520 525 530	1109
CAG GAC TCC TCT TCC TCA AAG GCC CCT CCC CCC AGC CTT CCA AGC CCA Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro 535 540 545	1157
TCC CGA CTC CCG GGG CCC TCG GAC ACC CCG ATC CTC CCA CAA TAA Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln 550 555 560	1202

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp 1 5 10 15
Leu Gln Glu Gly Ser Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile 20 25 30
His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr 35 40 45
Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg 50 55 60
Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His 65 70 75 80
Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile 85 90 95
Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn 100 105 110
Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys 115 120 125
Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln 130 135 140

Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu
 145 150 155 160
 Cys Val Ser Cys Ala Gly Ala Gly Pro Arg Cys Arg Pro Ile Asn Ala
 165 170 175
 Thr Leu Ala Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn
 180 185 190
 Thr Thr Ile Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln
 195 200 205
 Gly Val Leu Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val
 210 215 220
 Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro
 225 230 235 240
 Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg
 245 250 255
 Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys
 260 265 270
 Asp Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro
 275 280 285
 Ser Leu Pro Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile
 290 295 300
 Leu Pro Gln
 305

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1147 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 278..1132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCGAGATGGC TACAGGTAAG CGCCCCTAAA ATCCCTTTGG GCACAATGTG TCCTGAGGGG 60
 AGAGGCAGCG ACCTGTAGAT GGGACGGGGG CACTAACCCT CAGGTTTGGG GCTTTTGAAT 120
 GTGAGTATGG CCATGTAAGC CCAGTATTTG CCAATCTCA GAAAGCTCCT GGTCCCTGGA 180
 GGGATGGAGA GAGAAAAACA AACAGCTCCT GGAGCAGGGA CACTCCTGGC CTCTTGCTCT 240
 GCGGCTCCGT GTGTTGCCCT GTGGTTTCTC CCCACGC TCC CGG ACG TCC CTG CTC 295
 Ser Arg Thr Ser Leu Leu
 310
 CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT GCC 343
 Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala
 315 320 325

GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT TCG Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser 330 335 340 345	391
ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC TGT Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys 350 355 360	439
CCA GGC CCG GGG CAG GAT ACC GAC TGC AGG GAG TGT GAG AGC GGC TCC Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser 365 370 375	487
TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC AAA Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys 380 385 390	535
TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG GAC Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp 395 400 405	583
CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT TGG Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp 410 415 420 425	631
AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC ACC CTC TGC CTC AAT GGG Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Thr Leu Cys Leu Asn Gly 430 435 440	679
ACC GTG CAC CTC TCC TGT CAG GAG AAA CAG AAC ACC GTC TGC ACC TGC Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys 445 450 455	727
CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT AGT AAC His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn 460 465 470	775
TGT AAG AAA AGC CTG GAG TGC ACG AAG TTG TCC CTA CCC CAG ATT GAG Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Ser Leu Pro Gln Ile Glu 475 480 485	823
AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC ACA GCC GGT GCT GCC CCA Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Ala Gly Ala Ala Pro 490 495 500 505	871
GGT TGC CCA GAA TGC ACG CTA CAG GAA AAC CCA TTC TTC TCC CAG CCG Gly Cys Pro Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro 510 515 520	919
GGT GCC CCA ATA CTT CAG TGC ATG GGC TGC TGC TTC TCT AGA GCA TAT Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr 525 530 535	967
CCC ACT CCA CTA AGG TCC AAG AAG ACG ATG TTG GTC CAA AAG AAC GTC Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val 540 545 550	1015
ACC TCA GAG TCC ACT TGC TGT GTA GCT AAA TCA TAT AAC AGG GTC ACA Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr 555 560 565	1063
GTA ATG GGG GGT TTC AAA GTG GAG AAC CAC ACG GCG TGC CAC TGC AGT Val Met Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser 570 575 580 585	1111
ACT TGT TAT TAT CAC AAA TCT TAAGGATCCC TCGAG Thr Cys Tyr Tyr His Lys Ser 590	1147

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp
1 5 10 15
Leu Gln Glu Gly Ser Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile
20 25 30
His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr
35 40 45
Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg
50 55 60
Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His
65 70 75 80
Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile
85 90 95
Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn
100 105 110
Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys
115 120 125
Thr Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln
130 135 140
Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu
145 150 155 160
Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu
165 170 175
Ser Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr
180 185 190
Thr Ala Gly Ala Ala Pro Gly Cys Pro Glu Cys Thr Leu Gln Glu Asn
195 200 205
Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys
210 215 220
Cys Phe Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met
225 230 235 240
Leu Val Gln Lys Asn Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys
245 250 255
Ser Tyr Asn Arg Val Thr Val Met Gly Gly Phe Lys Val Glu Asn His
260 265 270
Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His Lys Ser
275 280 285

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 279..1287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTCGAGATGG CTACAGGTAA GCGCCCCTAA AATCCCTTTG GGCACAATGT GTCCTGAGGG	60
GAGAGGCAGC GACCTGTAGA TGGGACGGGG GACTAACCC TCAGGTTTGG GGCTTCTGAA	120
TGTGAGTATC GCCATGTAAG CCCAGTATTT GGCCAATGTC AGAAAGCTCC TGGTCCCTGG	180
AGGGATGGAG AGAGAAAAAC AAACACCTCC TGGAGCAGGG AGAGTGCTGC CCTCTTGCTC	240
TCCGGCTCCC TCTGTTGCCC TCTGGTTTCT CCCAGGC TCC CGG ACG TCC CTG	293
Ser Arg Thr Ser Leu	290
CTC CTG GCT TTT GGC CTG CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT	341
Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser	305
GCC GAT AGT GTG TGT CCC CAA GGA AAA TAT ATC CAC CCT CAA AAT AAT	389
Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn	320
TCG ATT TGC TGT ACC AAG TGC CAC AAA GGA ACC TAC TTG TAC AAT GAC	437
Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp	335
TGT CCA GGC CCG GGG CAG GAT ACG GAC TGC AGG GAG TGT GAG AGC GGC	485
Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly	350
TCC TTC ACC GCT TCA GAA AAC CAC CTC AGA CAC TGC CTC AGC TGC TCC	533
Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser	370
AAA TGC CGA AAG GAA ATG GGT CAG GTG GAG ATC TCT TCT TGC ACA GTG	581
Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val	385
GAC CGG GAC ACC GTG TGT GGC TGC AGG AAG AAC CAG TAC CGG CAT TAT	629
Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr	400
TGG AGT GAA AAC CTT TTC CAG TGC TTC AAT TGC AGC CTC TGC CTC AAT	677
Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn	415
GGG ACC GTG CAC CTC TCC TGC CAG GAG AAA CAG AAC ACC GTG TGC ACC	725
Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr	430
TGC CAT GCA GGT TTC TTT CTA AGA GAA AAC GAG TGT GTC TCC TGT AGT	773
Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser	450

AAC TGT AAG AAA AGC CTG GAG TGC ACG AAG TTG TGC CTA CCC CAG ATT Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile 455 460 465	821
GAG AAT GTT AAG GGC ACT GAG GAC TCA GGC ACC ACA GCT GGT GCT GGT Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr Ala Gly Ala Gly 470 475 480	869
CCA CGG TGC CGC CCC ATC AAT GCC ACC CTG GCT GTG GAG AAG GAG GGC Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala Val Glu Lys Glu Gly 485 490 495	917
TGC CCC GTG TGC ATC ACC GTC AAC ACC ACC ATC TGT GCC GGC TAC TGC Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala Gly Tyr Cys 500 505 510	965
CCC ACC ATG ACC CGC GTG CTG CAG GGG GTC CTG CCG GCC CTG CCT CAG Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala Leu Pro Gln 515 520 525 530	1013
GTG GTG TGC AAC TAC CGC GAT GTG CGC TTC GAG TCC ATC CGG CTC CCT Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile Arg Leu Pro 535 540 545	1061
GGC TGC CCG CGC GGC GTG AAC CCC GTG GTC TCC TAC GCC GTG GCT CTC Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser Tyr Ala Val Ala Leu 550 555 560	1109
AGC TGT CAA TGT GCA CTC TGC CGC CGC AGC ACC ACT GAC TGC GGG GGT Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr Thr Asp Cys Gly Gly 565 570 575	1157
CCC AAG GAC CAC CCC TTG ACC TGT GAT GAC CCC CGC TTC CAG GAC TCC Pro Lys Asp His Pro Leu Thr Cys Asp Asp Pro Arg Phe Gln Asp Ser 580 585 590	1205
TCT TCC TCA AAG GCC CCT CCC CCC AGC CTT CCA AGC CCA TCC CGA CTC Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser Pro Ser Arg Leu 595 600 605 610	1253
CCG GGG CCC TCG GAC ACC CCG ATC CTC CCA CAA T AAGGATCCCT CGAG Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln 615 620	1301

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu Pro Trp 1 5 10 15
Leu Gln Glu Gly Ser Ala Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile 20 25 30
His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr 35 40 45
Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg 50 55 60

Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu Arg His
 65 70 75 80
 Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile
 85 90 95
 Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn
 100 105 110
 Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys
 115 120 125
 Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln
 130 135 140
 Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu
 145 150 155 160
 Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu
 165 170 175
 Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr
 180 185 190
 Thr Ala Gly Ala Gly Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala
 195 200 205
 Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile
 210 215 220
 Cys Ala Gly Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu
 225 230 235 240
 Pro Ala Leu Pro Gln Val Val Cys Asn Tyr Arg Asp Val Arg Phe Glu
 245 250 255
 Ser Ile Arg Leu Pro Gly Cys Pro Arg Gly Val Asn Pro Val Val Ser
 260 265 270
 Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu Cys Arg Arg Ser Thr
 275 280 285
 Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp Asp Pro
 290 295 300
 Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro
 305 310 315 320
 Ser Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln
 325 330 335

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Gly Ala Ala Pro Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Gly Ala Gly

1

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTTCTCGAG ATGGCTACAG GTAAGCGCCC

30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ACCTGGGGCA GCACCGGCAC AGGAGACACA CTCGTTTTTC

39

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TGTGCCGGTG CTGCCCCAGG TTGCCAGAA TGCACGCTAC AG

42

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTTTGGATCC TTAAGATTTG TGATAATAAC AAGTAC

36

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCGTGGACCA GCACCAGCAC AGGAGACACA CTCGTTTTC

39

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TGTGCTGGTG CTGGTCCACG GTGCCGCCCC ATCAAT

36

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTTTGGATCC TTATTGTGGG AGGATCGGGG TG

32

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TTTTAGATCT CTTCTTGCAC AGTGGAC

27

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGTGGTGCCT GAGTCCTCAG T

21

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ACTGAGGACT CAGGCACCAC AGCCGGTGCT GCCCCAGGTT G

41

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TTTTTCTAGA GAAGCAGCAG CAGCCCATG

29

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTTCCACAG CCAGGGTGGC ATTGATGGGG CGGCACCGTG GACCAGCACC AGCTGTGGTG
CCTGAGTCCT CAGTG

60

75